

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/937,779B
Source: 1fw/b
Date Processed by STIC: 6/13/06

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779B

DATE: 06/13/2006
TIME: 09:45:31

Input Set : A:\00930003.APP
Output Set: N:\CRF4\06132006\I937779B.raw

3 <110> APPLICANT: DAHLQVIST, ANDERS
 4 STAHL, ULF
 5 LENMAN, MARIT
 6 BANAS, ANTONI
 7 RONNE, HANS
 8 STYMFNE, STEN
 10 <120> TITLE OF INVENTION: PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES
 11 THAT ENCODE PHOSPHOLIPID:DIACYLGLYCEROL
 12 ACYLTRANSFERASES
 14 <130> FILE REFERENCE: 0093/000003
 16 <140> CURRENT APPLICATION NUMBER: 09/937,779B
 17 <141> CURRENT FILING DATE: 2002-07-02
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP00/002701
 20 <151> PRIOR FILING DATE: 2000-03-28
 22 <150> PRIOR APPLICATION NUMBER: 60/180,687
 23 <151> PRIOR FILING DATE: 2000-02-07
 25 <150> PRIOR APPLICATION NUMBER: EP 99111321.8
 26 <151> PRIOR FILING DATE: 1999-06-10
 28 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
 29 <151> PRIOR FILING DATE: 1999-04-01
 31 <160> NUMBER OF SEQ ID NOS: 35
 33 <170> SOFTWARE: PatentIn Ver. 3.3
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1986
 37 <212> TYPE: DNA
 38 <213> ORGANISM: *Saccharomyces cerevisiae*
 40 <220> FEATURE:
 41 <221> NAME/KEY: CDS
 42 <222> LOCATION: (1)..(1983)
 44 <400> SEQUENCE: 1
 45 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 46 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 47 1 5 10 15
 49 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 50 Asp Glu Asn Asn Lys Gly Ser Val His Asn Lys Arg Glu Ser Arg
 51 20 25 30
 53 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 54 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 55 35 40 45
 57 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 58 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 59 50 55 60
 61 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240

P, 6

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62	Lys	Arg	Asp	Gly	Asn	Gly	Arg	Lys	Arg	Trp	Arg	Asp	Ser	Arg	Arg	Leu	
63	65						70				75					80	
65	att	tcc	att	ctt	ggt	gca	tcc	tta	ggt	gta	ctt	ttg	ccg	ttt	agc	ttt	288
66	Ile	Phe	Ile	Leu	Gly	Ala	Phe	Leu	Gly	Val	Leu	Leu	Pro	Phe	Ser	Phe	
67																95	
69	ggc	gct	tat	cat	gtt	cat	aat	agc	gat	agc	gac	ttg	ttt	gac	aac	ttt	336
70	Gly	Ala	Tyr	His	Val	His	Ser	Asn	Ser	Asp	Ser	Asp	Leu	Phe	Asp	Asn	Phe
71																110	
73	gta	aat	ttt	gat	tca	ctt	aaa	gtg	tat	ttg	gat	ttg	aaa	gat	ttt	384	
74	Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val	
75																125	
77	ctc	cca	caa	ggg	ata	agt	tcg	ttt	att	gat	gat	att	cag	gct	ggg	aac	432
78	Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn	
79																140	
81	tac	tcc	aca	tct	tct	tta	gat	gat	ctc	agt	gaa	aat	ttt	gcc	ttt	ggg	480
82	Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Asp	Leu	Ser	Glu	Asn	Phe	Ala	Val	Gly	
83																160	
85	aaa	caa	ctc	tta	cgt	gat	tat	aat	atc	gag	gcc	aaa	cat	cct	gtt	gta	528
86	Lys	Gln	Leu	Leu	Arg	Asp	Tyr	Asn	Ile	Glu	Ala	Lys	His	Pro	Val	Val	
87																165	
89	atg	gtt	cct	ggg	gtc	att	tct	acg	gga	att	gaa	agc	tgg	gga	gtt	att	576
90	Met	Val	Pro	Gly	Val	Ile	Ser	Thr	Gly	Ile	Glu	Ser	Trp	Gly	Val	Ile	
91																180	
93	gga	gac	gat	gag	tgc	gat	agt	tct	gcg	cat	ttt	cgt	aaa	cg	ctg	tgg	624
94	Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp	
95																195	
97	gga	agt	ttt	tac	atg	ctg	aga	aca	atg	gtt	atg	gat	aaa	gtt	tgt	tgg	672
98	Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp	
99																210	
101	ttg	aaa	cat	gta	atg	tta	gat	cct	gaa	aca	gg	ctg	gac	cca	ccg	aac	720
102	Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	
103																225	
105	ttt	acg	cta	cgt	gca	cag	ggc	tcc	gaa	tca	act	gat	tat	ttc	atc	768	
106	Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	
107																245	
109	gca	ggg	tat	tgg	att	tgg	aac	aaa	gtt	tcc	caa	aat	ctg	gga	gta	att	816
110	Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	
111																260	
113	ggc	tat	gaa	ccc	aat	aaa	atg	acg	agt	gct	gag	tat	gat	tgg	agg	ctt	864
114	Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	
115																275	
117	gca	tat	tta	gat	cta	gaa	aga	cgc	gat	agg	tac	ttt	acg	aag	cta	aag	912
118	Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys	
119																290	
121	gaa	caa	atc	gaa	ctg	ttt	cat	caa	ttg	agt	gg	aaa	gtt	tgt	tta	960	
122	Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu	
123																305	
125	att	gga	cat	tct	atg	gg	tct	cag	att	atc	ttt	tac	ttt	atg	aaa	tgg	1008
126	Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp	

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127	325	330	335	
129	gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt			1056
130	Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val			
131	340	345	350	
133	aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc			1104
134	Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly			
135	355	360	365	
137	gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc			1152
138	Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr			
139	370	375	380	
141	att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca			1200
142	Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser			
143	385	390	395	400
145	aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca			1248
146	Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser			
147	405	410	415	
149	atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct			1296
150	Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser			
151	420	425	430	
153	tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att			1344
154	Ser Glu Asp Ala Leu Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile			
155	435	440	445	
157	cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg			1392
158	Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met			
159	450	455	460	
161	aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa			1440
162	Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln			
163	465	470	475	480
165	aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa			1488
166	Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu			
167	485	490	495	
169	gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg			1536
170	Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met			
171	500	505	510	
173	gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac			1584
174	Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr			
175	515	520	525	
177	ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat			1632
178	Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp			
179	530	535	540	
181	gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct			1680
182	Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro			
183	545	550	555	560
185	gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca			1728
186	Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser			
187	565	570	575	
189	atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga			1776
190	Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly			
191	580	585	590	

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193 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 194 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 195 595 600 605
 197 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 198 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 199 610 615 620
 201 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 202 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 203 625 630 635 640
 205 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 206 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 207 645 650 655
 209 atg ccc ttc cca atg taa 1986
 210 Met Pro Phe Pro Met
 211 660
 214 <210> SEQ ID NO: 2
 215 <211> LENGTH: 661
 216 <212> TYPE: PRT
 217 <213> ORGANISM: *Saccharomyces cerevisiae*
 219 <400> SEQUENCE: 2
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 221 1 5 10 15
 223 Asp Glu Asn Asn Lys Gly Ser Val His Asn Lys Arg Glu Ser Arg
 224 20 25 30
 226 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 227 35 40 45
 229 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 230 50 55 60
 232 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 233 65 70 75 80
 235 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 236 85 90 95
 238 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 239 100 105 110
 241 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 242 115 120 125
 244 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 245 130 135 140
 247 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 248 145 150 155 160
 250 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 251 165 170 175
 253 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 254 180 185 190
 256 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 257 195 200 205
 259 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 260 210 215 220
 262 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn

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263	225	230	235	240												
265	Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile
266																255
268																
269																270
271	Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu
272																285
274																
275																
277	Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu
278																320
280																
281																335
283	Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val
284																350
286	Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly
287																365
289	Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr
290																380
292	Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser
293																400
295	Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser
296																415
298	Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser
299																430
301	Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile
302																445
304	Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met
305																460
307	Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln
308																480
310	Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu
311																495
313	Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met
314																510
316	Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr
317																525
319	Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp
320																540
322	Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro
323																560
325	Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser
326																575
328	Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly
329																590
331	Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp
332																605
334	Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser
335																620

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2363
Seq#:7; N Pos. 601,627
Seq#:9; N Pos. 15,45,83,103,107,112,210
Seq#:25; N Pos. 240,385
Seq#:25; Xaa Pos. 41,89
Seq#:26; N Pos. 601,627
Seq#:28; N Pos. 15,45,83,103,107,112,210
Seq#:32; Xaa Pos. 2
Seq#:35; Xaa Pos. 41,89

VERIFICATION SUMMARY

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L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:565
M:341 Repeated in SeqNo=7
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
M:341 Repeated in SeqNo=25
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:565
M:341 Repeated in SeqNo=26
L:2482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:2636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:2689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:32
M:341 Repeated in SeqNo=35